

Applicant : Michael A. Apicella et al.
Serial No. : 09/574,460
Filed : May 18, 2000
Page : 2 of 7

Attorney's Docket No.: 17023.004US1 / 98010

Amendments to the Claims:

1-29. (Cancelled)

30. (Currently amended) A process for the production of a *Haemophilus influenzae*-specific lipooligosaccharide (LOS) which comprises the steps of:

(a) growing in a culture medium gram-negative bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding ~~comprising~~ an ~~Undecaprenyl~~ Undecaprenyl-phosphate (~~UDP~~) N-acetyl glucosaminyl ~~glucosamine~~ (~~GlcNAc~~); ~~Undecaprenol GlcNAc 1-phosphate transferase (*rfe*) gene~~, and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (~~*lsgG*~~) ~~gene product~~ (*LsgG*) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by *LsgG* such that a *H. influenzae*-specific LOS is synthesized by the addition of an acceptor molecule to the terminal heptose molecule; and

(b) recovering the *H. influenzae*-specific LOS from the culture medium.

31. (Previously presented) The process of claim 30, wherein the bacteria are *Escherichia coli*.

32. (Previously presented) The process of claim 31, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

33. (Previously presented) The process of claim 30, wherein the bacteria are *Salmonella minnesota*.

34. (Previously presented) The process of claim 30, wherein the acceptor molecule is N-acetylglucosamine.

35. (Currently amended) The process of claim 30, wherein the DNA sequence encoding *rfe* ~~gene~~ is from *Haemophilus influenzae*.

Applicant : Michael A. Apicella et al.
Serial No. : 09/574,460
Filed : May 18, 2000
Page : 3 of 7

Attorney's Docket No.: 17023.004US1 / 98010

36. (Currently amended) The process of claim 30, wherein the DNA sequence encoding comprising a *rfe* gene is part of the gram-negative bacterial genome.
37. (Currently amended) The process of claim 30, wherein the isolated DNA sequence encoding the *lsgG* LsgG is ~~contained~~ comprised in a vector.
38. (Previously presented) The process of claim 30, wherein the bacteria further comprise a glycosyltransferase.
39. (Currently amended) A process for the production of a complex carbohydrate comprising the steps of:
- (a) growing in a culture medium gram-negative bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding comprising an UndecaprenylUndecaprenyl-phosphate (UDP) N-acetyl glucosaminyl glucosamine (GlcNAc):Undecaprenol GlcNAc-1 phosphate transferase (*rfe*) gene, and (iii) an isolated DNA sequence encoding a liposaccharide-synthesis gene G polypeptide (*lsgG*) gene-product (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* gene is regulated by LsgG such that a complex carbohydrate is synthesized by the addition of an acceptor molecule to the heptose molecule; and
 - (b) recovering the complex carbohydrate from the culture medium.
40. (Previously presented) The process of claim 39, wherein the bacteria are *Escherichia coli*.
41. (Previously presented) The process of claim 40, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.
42. (Previously presented) The process of claim 39, wherein the bacteria are *Salmonella minnesota*.

Applicant : Michael A. Apicella et al.
Serial No. : 09/574,460
Filed : May 18, 2000
Page : 4 of 7

Attorney's Docket No.: 17023.004US1 / 98010

43. (Previously presented) The process of claim 39, wherein the acceptor molecule is N-acetylglucosamine.
44. (Currently amended) The process of claim 39, wherein the DNA sequence encoding *rfe* gene is from *Haemophilus influenzae*.
45. (Currently amended) The process of claim 39, wherein the DNA sequence encoding comprising a *rfe* gene is part of the gram-negative bacterial genome.
46. (Currently amended) The process of claim 39, wherein the isolated DNA sequence encoding *LsgG* comprising the *LsgG* is contained in a vector.
47. (Previously presented) The process of claim 39, wherein the bacteria further comprise a glycosyltransferase.
48. (Currently amended) A method of modifying a terminal heptose of a lipopolysaccharide (LPS) or lipooligosaccharide (LOS) core structure of a gram-negative bacterial species comprising a polynucleotide encoding containing an Undecaprenyl Undecaprenyl-phosphate (UDP) N-acetyl glucosaminyl glucosamine (GlcNAc):Undecaprenol GlcNAc-1-phosphate transferase (*rfe*), wherein gene comprising regulating the polynucleotide encoding *rfe* is regulated by gene with a protein encoded by an isolated lipooligosaccharide-synthesis gene G polypeptide (*LsgG*) (~~*logG*~~) gene from *Haemophilus influenzae* such that an N-acetyl glucosamine is added onto the terminal heptose.
49. (Previously presented) The method of claim 48 wherein the bacteria are *Escherichia coli*.
50. (Previously presented) The method of claim 49, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

Applicant : Michael A. Apicella et al.
Serial No. : 09/574,460
Filed : May 18, 2000
Page : 5 of 7

Attorney's Docket No.: 17023.004US1 / 98010

51. (Previously presented) The method of claim 48, wherein the bacteria are *Salmonella minnesota*.
52. (Currently amended) The method of claim 48, wherein the polynucleotide encoding rfe gene is from *Haemophilus influenzae*.
53. (Currently amended) The method of claim 48, wherein the polynucleotide encoding rfe gene is part of the gram-negative bacterial genome.
54. (Currently amended) The method of claim 48, wherein ~~the~~ a polynucleotide encoding the LsgG isolated ~~lsgG~~ gene is comprised ~~contained~~ in a vector.
55. (Previously presented) The method of claim 48, wherein the bacteria further comprise a glycosyltransferase.